



Application Number

IDS Flag Clearance for Application

IDS Information

Content	Mailroom Date	Entry Number	IDS Review	Reviewer
M844	11-24-2004	16	<input checked="" type="checkbox"/>	12-16-2004 13:56:16 gtrammell
M844	01-27-2004	21	<input checked="" type="checkbox"/>	01-03-2006 07:37:32 YPak

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Database : A_Geneseq_21:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query				Description
	Score	Match	Length	DB ID	
1	1298	100.0	254	4 AAB47522	Aab47522 (R)-2-oct
2	944	72.7	254	4 AAB49773	Aab49773 Protein w
3	586.5	45.2	257	7 ADF06077	Adf06077 Bacterial
4	582.5	44.9	248	6 ADB06934	Adb06934 Alloiococ
5	582.5	44.9	281	6 ADB06936	Adb06936 Alloiococ
6	574.5	44.3	246	8 ADN17584	Adn17584 Bacterial
7	505.5	38.9	261	6 ABU29919	Abu29919 Protein e
8	498.5	38.4	261	5 AAE20115	Aae20115 Lactobaci
9	496.5	38.3	261	9 ADZ77293	Adz77293 Bacillus
10	495.5	38.2	261	9 ADZ77291	Adz77291 Bacillus
11	495.5	38.2	261	9 ADZ77289	Adz77289 Bacillus
12	495.5	38.2	261	9 ADZ77283	Adz77283 Bacillus
13	494.5	38.1	261	3 AAY96271	Aay96271 B. subtil
14	494.5	38.1	261	3 AAY54424	Aay54424 Amino aci

RESULT 1

AAB47522

ID AAB47522 standard; protein; 254 AA.

XX

AC AAB47522;

XX

DT 04-DEC-2001 (first entry)

XX

DE (R)-2-octanol dehydrogenase.

XX

KW (R)-2-octanol dehydrogenase; ketone; alcohol; beta-NAD; co-enzyme;

KW oxidize; optical isomer; (R)-2-octanol; 4-haloacetoacetate ester;

KW (S)-4-halo-3-hydroxybutyrate ester; HMG-CoA reductase inhibitor;

KW D-carnitine; (R)-propoxybenzene.

XX

OS Pichia finlandica.

XX

PN WO200161014-A1.

XX

PD 23-AUG-2001.

XX

PF 15-FEB-2001; 2001WO-JP001082.

XX

PR 16-FEB-2000; 2000JP-00043506.

PR 08-DEC-2000; 2000JP-00374593.

XX

PA (DAIICHI) DAICEL CHEM IND LTD.

XX

PI Kudoh M, Yamamoto H;

XX

DR WPI; 2001-596701/67.

DR N-PSDB; AAH43472.

XX

PT (R)-2-octanol dehydrogenase for producing intermediates for HMG-CoA
PT reductase inhibitors or D-carnitine.

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PS Claim 9; Page 83-85; 97pp; Japanese.

XX

CC This sequence represents (R)-2-octanol dehydrogenase which has the
CC following characteristics: (1) produces ketones by oxidizing alcohol
CC using beta-NAD as a co-enzyme; and produces alcohols by reducing ketones
CC using beta-NADH as a co-enzyme; and (2) preferentially oxidizes the
CC optical isomer (R)-2-octanol; and reduces 4-haloacetoacetate ester to
CC produce (S)-4-halo-3-hydroxybutyrate ester. (S)-4-halo-3-hydroxybutyrate
CC esters are useful as intermediates for HMG-CoA reductase inhibitors or D-
CC carnitine. (R)-propoxybenzene derivatives are particularly useful as
CC intermediates for optical isomers of ofloxane ((S)-(-)-9-fluoro-3-methyl-
CC 10-(4-methyl-1-piperazinyl)-7-oxo-2,3-dihydro-7H-pyrido(1,2,3-de)(1,4)
CC benzo(d)azin-6-carboxylic acid)

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SQ Sequence 254 AA;

Query Match 100.0%; Score 1298; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.9e-119;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSYNFHNKVAVVTGALSGIGLSVAKKFLQLGAKVTISDVSGEKKYHETVVALKAQNLNTD 60

Db 1 ||||||| MSYNFHNKVAVVTGALSGIGLSVAKKFLQLGAKVTISDVSGEKKYHETVVALKAQNLNTD 60

Qy 61 NLHYVQADSSKEEDNKKLisetLATFGGLDIVCANAGIGKFAPTHETPFDVWKVIAVNL 120
|||
Db 61 NLHYVQADSSKEEDNKKLisetLATFGGLDIVCANAGIGKFAPTHETPFDVWKVIAVNL 120

Qy 121 NGVFLLDKLAINYWLEKSKPGVIVNMGSVHSFVAAPGLAHYGAAKGGVKLLTQTLALEYA 180
|||
Db 121 NGVFLLDKLAINYWLEKSKPGVIVNMGSVHSFVAAPGLAHYGAAKGGVKLLTQTLALEYA 180

Qy 181 SHGIRVNSVNPYISTPLIDEVPKERLDKLVLSPHPIGRRLRPEEVADAVAFLCSQEATFI 240
|||
Db 181 SHGIRVNSVNPYISTPLIDEVPKERLDKLVLSPHPIGRRLRPEEVADAVAFLCSQEATFI 240

Qy 241 NGVSLPVDGYYTAQ 254
|||
Db 241 NGVSLPVDGYYTAQ 254

RESULT 2

AAB49773

ID AAB49773 standard; protein; 254 AA.

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AC AAB49773;

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DT 23-APR-2001 (first entry)

XX

DE Protein with acetylpyridine derivative reducing action.

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KW Optically-active pyridineethanol derivative; asymmetric reduction.

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OS Candida maris.

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PN WO200105996-A1.

XX

PD 25-JAN-2001.

XX

PF 28-JUN-2000; 2000WO-JP004237.

XX

PR 21-JUL-1999; 99JP-00206503.

XX

PA (KANF) KANEKA CORP.

XX

PI Kawano S, Horikawa M, Yasohara Y, Hasegawa J;

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DR WPI; 2001-159546/16.

DR N-PSDB; AAF29375, AAF29376.

XX

PT Efficient, high-yielding preparation of optically-active pyridineethanol derivatives by stereoselectively reducing acetylpyridine derivatives e.g. with enzyme having asymmetric reduction activity, for pharmaceutical intermediates.

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PS Claim 14; Fig 1; 76pp; Japanese.

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CC This invention relates to a process for producing optically-active

CC pyridineethanol derivatives by stereoselectively reducing acetylpyridine
CC derivatives with an enzyme or enzyme source having asymmetric reduction
CC activity. The process is efficient and high yielding to give R and S
CC isomers by suitable manipulation. The method is for the preparation of
CC optically-active pyridineethanol derivatives by stereoselectively
CC reducing acetylpyridine derivatives, and also similarly for their
CC polycyclic analogues, for use as pharmaceutical and agrochemical
CC intermediates, as well as in fine chemical production. The present
CC sequence represents the amino acid sequence of the enzyme used in the
CC process which has acetylpyridine derivative reducing action

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SQ Sequence 254 AA;

Query Match 72.7%; Score 944; DB 4; Length 254;
Best Local Similarity 69.7%; Pred. No. 2.4e-84;
Matches 177; Conservative 36; Mismatches 41; Indels 0; Gaps 0;

Qy 1 MSYNFHNKVAVTGALSGIGLSVAKKFLQLGAKVTISDVSGEKKYHETVVALKAQNLNTD 60
||| || | : ||| ||| ||| : ||| ||| ||| ||| : | : ||| : | | : ::

Db 1 MSYNFANKVLIVTGGLSGIGLAVAKKFLQLGAKVTISDI SATEKYNTVVGEFKTEGIDVK 60

Qy 61 NLHYVQADSSKEEDNKKLISETLATFGGLDIVCANAGIGKFAPTHETPDFDVKKVIAVNL 120
| : | : ||| : ||| ||| : ||| ||| ||| | | : : ||| : ||| : ::||

Db 61 NVQYIQADASKEADNEKLISETLSAFGDLDYVCANAGIATFTQTTDISYDVWRKVTSINL 120

Qy 121 NGVFLLDKLAINYWLEKSKPGVIVNMGSVHSFVAAPGLAHYGAAKGGVKLLTQTLALEYA 180
: ||| : ||| | : | : ||| ||| : ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||

Db 121 DGVFMLDKLAAQYFLSKNKGAIVNMGSIHSYVAAPGLSHYGAAKGGLKLLTQTMALLEYA 180

Qy 181 SHGIRVNSVNPYI STPLIDEVPKERLDKLVLHPIGRILGRPEEVADAFLCSQEATFI 240
: ||| ||| ||| ||| | : | : ||| : ||| : ||| ||| ||| : ||| ||| ||| |||

Db 181 AKGIRVNSVNPYIKTPLLDICPKEHMDYLITQHPIGRLGKPEEIASAVAFLCSDEATFI 240

Qy 241 NGVSLPVDGYYTAQ 254
|| : | | | | | | :

Db 241 NGISLLVDGGYTAR 254

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

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SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	
1	1298	100.0	254	2	US-09-978-758-2 Sequence 2, Appli
2	586.5	45.2	257	2	US-09-543-681A-6362 Sequence 6362, Ap
3	503.5	38.8	309	2	US-09-248-796A-16823 Sequence 16823, A
4	494.5	38.1	261	2	US-09-468-738A-29 Sequence 29, Appl
5	494.5	38.1	261	2	US-09-940-019-29 Sequence 29, Appl
6	494.5	38.1	261	2	US-09-940-037A-29 Sequence 29, Appl
7	494.5	38.1	261	2	US-09-305-390-18 Sequence 18, Appl
8	477.5	36.8	263	2	US-09-710-279-204 Sequence 204, App
9	472.5	36.4	267	2	US-09-134-001C-5042 Sequence 5042, Ap
10	470.5	36.2	251	2	US-09-648-004-20 Sequence 20, Appl
11	470.5	36.2	251	2	US-10-272-419-20 Sequence 20, Appl
12	453.5	34.9	261	2	US-10-004-115B-36 Sequence 36, Appl
13	440	33.9	252	2	US-08-822-322-8 Sequence 8, Appli
14	440	33.9	252	2	US-09-466-109-8 Sequence 8, Appli
15	425	32.7	277	2	US-09-543-681A-8037 Sequence 8037, Ap

Database : UniProt_05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	619.5	47.7	247	2	Q81AU6_BACCR	Q81au6 bacillus ce
2	577	44.5	246	2	Q8G0H2_BRUSU	Q8g0h2 brucella su
3	511.5	39.4	262	2	Q5A1C0_CANAL	Q5a1c0 candida alb
4	504.5	38.9	262	2	Q5FK32_LACAC	Q5fk32 lactobacill
5	494.5	38.1	261	1	DHG_BACSU	P12310 bacillus su
6	491.5	37.9	261	1	DHGA_BACME	P10528 bacillus me
7	490	37.8	244	2	Q8ELC2_OCEIH	Q8elc2 oceanobacil
8	488.5	37.6	261	1	DHG4_BACME	P39485 bacillus me
9	485.5	37.4	261	2	Q632X4_BACCZ	Q632x4 bacillus ce
10	484.5	37.3	261	2	Q81KM8_BACAN	Q81km8 bacillus an
11	482.5	37.2	261	1	DHG3_BACME	P39484 bacillus me
12	478.5	36.9	261	2	Q4MVK1_BACCE	Q4mvk1 bacillus ce
13	478.5	36.9	263	2	Q5HLZ1_STAEQ	Q5hlz1 staphylococ
14	477.5	36.8	261	1	DHG2_BACME	P39483 bacillus me
15	477.5	36.8	261	2	Q6HCG4_BACHK	Q6hcg4 bacillus th
16	477.5	36.8	261	2	Q9F2A6_BACLI	Q9f2a6 bacillus li
17	477.5	36.8	261	2	Q65HM4_BACLD	Q65hm4 bacillus li
18	474.5	36.6	261	2	Q5BMD7_BACME	Q5bmd7 bacillus me
19	473.5	36.5	259	2	Q831W5_ENTFA	Q831w5 enterococcu
20	473.5	36.5	261	2	Q5BMD8_BACME	Q5bmd8 bacillus me

Database : PIR_80:
 1: pir1:
 2: pir2:
 3: pir3:
 4: pir4:

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SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	494.5	38.1	261	2	D69629	glucose 1-dehydrog
2	491.5	37.9	261	1	S00812	glucose 1-dehydrog
3	488.5	37.6	261	2	I40225	glucose 1-dehydrog
4	482.5	37.2	261	2	I40224	glucose 1-dehydrog
5	477.5	36.8	261	2	I39853	glucose 1-dehydrog
6	471.5	36.3	255	1	S39737	glucose 1-dehydrog
7	455.5	35.1	261	2	A33528	glucose 1-dehydrog
8	454.5	35.0	261	2	JS0385	glucose 1-dehydrog
9	448	34.5	262	2	S02299	glucose 1-dehydrog
10	448	34.5	272	2	AG3359	glucose 1-dehydrog
11	446.5	34.4	263	2	S01227	glucose 1-dehydrog
12	422.5	32.6	255	2	G82644	2,5-dichloro-2,5-c
13	420.5	32.4	258	2	G69755	glucose 1-dehydrog
14	418.5	32.2	269	2	AE2285	glucose 1-dehydrog
15	413.5	31.9	250	1	S47054	probable dehydroge
16	404.5	31.2	251	2	G72389	oxidoreductase, sh
17	396	30.5	246	2	A69621	3-oxoacyl-[acyl-ca
18	395.5	30.5	245	2	AE3517	3-oxoacyl-(acyl-ca
19	393	30.3	257	2	A72395	oxidoreductase, sh
20	391.5	30.2	271	2	AG3285	3-hydroxybutyrate